

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: Adams, Camilia W.
Ashkenazi, Avi J.
Chuntharapai, Anan
Kim, Kyung J.

10 (ii) TITLE OF INVENTION: Apo-2 Receptor

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: Genentech, Inc.
(B) STREET: 1 DNA Way
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
20 (F) ZIP: 94080

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
30 (B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Marschang, Diane L.
35 (B) REGISTRATION NUMBER: 35,600
(C) REFERENCE/DOCKET NUMBER: P1101R2

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 650/225-5416
40 (B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 411 amino acids
45 (B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

50 Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg
1 5 10 15

Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro
20 25 30

55 Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val
35 40 45

Leu Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp
60 50 55 60

Leu Ala Pro Gln Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser
65 70 75

Pro Ser Glu Gly Leu Cys Pro Pro Gly His His Ile Ser Glu Asp
80 85 90

5 Gly Arg Asp Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr
95 100 105

His Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys Asp
110 115 120

10 Ser Gly Glu Val Glu Leu Ser Pro Cys Thr Thr Thr Arg Asn Thr
125 130 135

Val Cys Gln Cys Glu Glu Gly Thr Phe Arg Glu Glu Asp Ser Pro
140 145 150

15 Glu Met Cys Arg Lys Cys Arg Thr Gly Cys Pro Arg Gly Met Val
155 160 165

20 Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile Glu Cys Val His
170 175 180

Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala Val Val
185 190 195

25 Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys
200 205 210

Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly Asp
215 220 225

30 Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp
230 235 240

35 Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val
245 250 255

Pro Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly
260 265 270

40 Val Asn Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro
275 280 285

Ala Glu Ala Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala
290 295 300

45 Asn Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp
305 310 315

Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg
320 325 330

50 Lys Leu Gly Leu Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu
335 340 345

55 Ala Ala Gly His Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp
350 355 360

Val Asn Lys Thr Gly Arg Asp Ala Ser Val His Thr Leu Leu Asp
365 370 375

60 Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu
380 385 390

Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn

Ala Asp Ser Ala Xaa Ser
410 411

5

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1799 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

15

CCCACGCGTC CGCATAAATC AGCACGCGGC CGGAGAACCC CGCAATCTCT 50

GCGCCACAA AATACACCGA CGATGCCCCG TCTACTTTAA GGGCTGAAAC 100

20

CCACGGGCCT GAGAGACTAT AAGAGCGTTC CCTACCGCC ATG GAA 145
Met Glu
1

25

CAA CGG GGA CAG AAC GCC CCG GCC GCT TCG GGG GCC CGG 184
Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg
5 10 15

30

AAA AGG CAC GGC CCA GGA CCC AGG GAG GCG CGG GGA GCC 223
Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala
20 25

35

AGG CCT GGG CTC CGG GTC CCC AAG ACC CTT GTG CTC GTT 262
Arg Pro Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val
30 35 40

40

GTC GCC GCG GTC CTG CTG TTG GTC TCA GCT GAG TCT GCT 301
Val Ala Ala Val Leu Leu Leu Val Ser Ala Glu Ser Ala
45 50

45

CTG ATC ACC CAA CAA GAC CTA GCT CCC CAG CAG AGA GCG 340
Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln Gln Arg Ala
55 60 65

50

GCC CCA CAA CAA AAG AGG TCC AGC CCC TCA GAG GGA TTG 379
Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
70 75 80

TGT CCA CCT GGA CAC CAT ATC TCA GAA GAC GGT AGA GAT 418
Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp
85 90

55

TGC ATC TCC TGC AAA TAT GGA CAG GAC TAT AGC ACT CAC 457
Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His
95 100 105

60

TGG AAT GAC CTC CTT TTC TGC TTG CGC TGC ACC AGG TGT 496
Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys
110 115

GAT TCA GGT GAA GTG GAG CTA AGT CCC TGC ACC ACG ACC 535
Asp Ser Gly Glu Val Glu Leu Ser Pro Cys Thr Thr Thr
120 125 130

AGA AAC ACA GTG TGT CAG TGC GAA GAA GGC ACC TTC CGG 574
Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe Arg
135 140 145

5 GAA GAA GAT TCT CCT GAG ATG TGC CGG AAG TGC CGC ACA 613
Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr
150 155

10 GGG TGT CCC AGA GGG ATG GTC AAG GTC GGT GAT TGT ACA 652
Gly Cys Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr
160 165 170

15 CCC TGG AGT GAC ATC GAA TGT GTC CAC AAA GAA TCA GGC 691
Pro Trp Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly
175 180

20 ATC ATC ATA GGA GTC ACA GTT GCA GCC GTA GTC TTG ATT 730
Ile Ile Ile Gly Val Thr Val Ala Ala Val Val Leu Ile
185 190 195

25 GTG GCT GTG TTT GTT TGC AAG TCT TTA CTG TGG AAG AAA 769
Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys
200 205 210

30 GTC CTT CCT TAC CTG AAA GGC ATC TGC TCA GGT GGT GGT 808
Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly
215 220

35 GGG GAC CCT GAG CGT GTG GAC AGA AGC TCA CAA CGA CCT 847
Gly Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro
225 230 235

40 GGG GCT GAG GAC AAT GTC CTC AAT GAG ATC GTG AGT ATC 886
Gly Ala Glu Asp Asn Val Leu Asn Glu Ile Val Ser Ile
240 245

45 TTG CAG CCC ACC CAG GTC CCT GAG CAG GAA ATG GAA GTC 925
Leu Gln Pro Thr Gln Val Pro Glu Gln Glu Met Glu Val
250 255 260

50 CAG GAG CCA GCA GAG CCA ACA GGT GTC AAC ATG TTG TCC 964
Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Met Leu Ser
265 270 275

55 CCC GGG GAG TCA GAG CAT CTG CTG GAA CCG GCA GAA GCT 1003
Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala
280 285

60 GAA AGG TCT CAG AGG AGG AGG CTG CTG GTT CCA GCA AAT 1042
Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn
290 295 300

GAA GGT GAT CCC ACT GAG ACT CTG AGA CAG TGC TTC GAT 1081
Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp
305 310

GAC TTT GCA GAC TTG GTG CCC TTT GAC TCC TGG GAG CCG 1120
Asp Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro
315 320 325

CTC ATG AGG AAG TTG GGC CTC ATG GAC AAT GAG ATA AAG 1159
Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile Lys
330 335 340

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GTG GCT AAA GCT GAG GCA GCG GGC CAC AGG GAC ACC TTG 1198
Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu
345 350

5 TAC ACG ATG CTG ATA AAG TGG GTC AAC AAA ACC GGG CGA 1237
Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg
355 360 365

10 GAT GCC TCT GTC CAC ACC CTG CTG GAT GCC TTG GAG ACG 1276
Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr
370 375

15 CTG GGA GAG AGA CTT GCC AAG CAG AAG ATT GAG GAC CAC 1315
Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His
380 385 390

20 TTG TTG AGC TCT GGA AAG TTC ATG TAT CTA GAA GGT AAT 1354
Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn
395 400 405

GCA GAC TCT GCC WTG TCC TAAGTGTG ATTCTCTTCA GGAAGTGAGA 1400
Ala Asp Ser Ala Xaa Ser
410 411

25 CCTTCCCTGG TTTACCTTTT TTCTGGAAAA AGCCCAACTG GACTCCAGTC 1450

AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC 1500

30 CCATCCAACA TCACCCAGTG GATGGAACAT CCTGTAACTT TTTACTGCAC 1550

TTGGCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAAT 1600

GTCTGGATCA TTCCGTTTGT GCGTACTTTG AGATTTGGTT TGGGATGTCA 1650

35 TTGTTTTTAC AGCACTTTTT TATCCTAATG TAAATGCTTT ATTTATTTAT 1700

TTGGGCTACA TTGTAAGATC CATCTACAAA AAAAAAAAAA AAAAAAAAAAG 1750

GCGCGCCGCG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC 1799

40

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 70 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

50

GGGAGCCGCT CATGAGGAAG TTGGGCCTCA TGGACAATGA GATAAAGGTG 50

GCTAAAGCTG AGGCAGCGGG 70

55

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 29 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

5 (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

15

AGGATGGGAA GTGTGTGATA TATCCTTGAT 30

(2) INFORMATION FOR SEQ ID NO:6:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATG ACC ATG ATT ACG CCA AGC TTT GGA GCC TTT TTT 36
 Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe
 1 5 10

TTG GAG ATT TTC AAC GTG AAA AAA TTA TTA TTC GCA ATT 75
 Leu Glu Ile Phe Asn Val Lys Lys Leu Leu Phe Ala Ile
 15 20 25

CCT TTA GTT GTT CCT TTC TAT GCG GCC CAG CCG GCC ATG 114
 Pro Leu Val Val Pro Phe Tyr Ala Ala Gln Pro Ala Met
 30 35

GCC GAG GTG CAG CTG GTG CAG TCT GGG GGA GGT GTG GAA 153
 Ala Glu Val Gln Leu Val Gln Ser Gly Gly Gly Val Glu
 40 45 50

CGG CCG GGG GGG TCC CTG AGA CTC TCC TGT GCA GCC TCT 192
 Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
 55 60

GGA TTC ACC TTT GAT GAT TAT GGC ATG AGC TGG GTC CGC 231
 Gly Phe Thr Phe Asp Tyr Gly Met Ser Trp Val Arg
 65 70 75

CAA GCT CCA GGG AAG GGG CTG GAG TGG GTC TCT GGT ATT 270
 Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile
 80 85 90

AAT TGG AAT GGT GGT AGC ACA GGA TAT GCA GAC TCT GTG 309
 Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val
 95 100

60

AAG GGC CGA GTC ACC ATC TCC AGA GAC AAC GCC AAG AAC 348
 Lys Gly Arg Val Thr Ile Ser Arg Asp Asn Ala Lys Asn
 105 110 115

TCC CTG TAT CTG CAA ATG AAC AGC CTG AGA GCC GAG GAC 387
 Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
 120 125

5 ACG GCC GTA TAT TAC TGT GCG AAA ATC CTG GGT GCC GGA 426
 Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala Gly
 130 135 140

10 CGG GGC TGG TAC TTC GAT CTC TGG GGG AAG GGG ACC ACG 465
 Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr
 145 150 155

15 GTC ACC GTC TCG AGT GGT GGA GGC GGT TCA GGC GGA GGT 504
 Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 160 165

20 GGC AGC GGC GGT GGC GGA TCG TCT GAG CTG ACT CAG GAC 543
 Gly Ser Gly Gly Gly Gly Ser Ser Glu Leu Thr Gln Asp
 170 175 180

CCT GCT GTG TCT GTG GCC TTG GGA CAG ACA GTC AGG ATC 582
 Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile
 185 190

25 ACA TGC CAA GGA GAC AGC CTC AGA AGC TAT TAT GCA AGC 621
 Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser
 195 200 205

30 TGG TAC CAG CAG AAG CCA GGA CAG GCC CCT GTA CTT GTC 660
 Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val
 210 215 220

35 ATC TAT GGT AAA AAC AAC CGG CCC TCA GGG ATC CCA GAC 699
 Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp
 225 230

40 CGA TTC TCT GGC TCC AGC TCA GGA AAC ACA GCT TCC TTG 738
 Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu
 235 240 245

ACC ATC ACT GGG GCT CAG GCG GAA GAT GAG GCT GAC TAT 777
 Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr
 250 255

45 TAC TGT AAC TCC CGG GAC AGC AGT GGT AAC CAT GTG GTA 816
 Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val Val
 260 265 270

50 TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA GGT GCG GCC 855
 Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala Ala
 275 280 285

55 GCA CAT CAT CAT CAC CAT CAC GGG GCC GCA GAA CAA AAA 894
 Ala His His His His His His Gly Ala Ala Glu Gln Lys
 290 295

60 CTC ATC TCA GAA GAG GAT CTG AAT GGG GCC GCA TAG 930
 Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala
 300 305 309

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 939 base pairs

(B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

	ATG ACC ATG ATT ACG CCA AGC TTT GGA GCC TTT TTT	36
	Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe	
10	1 5 10	
	TTG GAG ATT TTC AAC GTG AAA AAA TTA TTA TTC GCA ATT	75
	Leu Glu Ile Phe Asn Val Lys Lys Leu Leu Phe Ala Ile	
	15 20 25	
15	CCT TTA GTT GTT CCT TTC TAT GCG GCC CAG CCG GCC ATG	114
	Pro Leu Val Val Pro Phe Tyr Ala Ala Gln Pro Ala Met	
	30 35	
20	GCC GGG GTG CAG CTG GTG GAG TCT GGG GGA GGC TTG GTC	153
	Ala Gly Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val	
	40 45 50	
	CAG CCT GGG GGG TCC CTG AGA CTC TCC TGT GCA GCC TCT	192
25	Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser	
	55 60	
	GGA TTC ACC TTT AGT AGC TAT TGG ATG AGC TGG GTC CGC	231
	Gly Phe Thr Phe Ser Ser Tyr Trp Met Ser Trp Val Arg	
30	65 70 75	
	CAG GCT CCA GGG AAG GGG CTG GAG TGG GTG GCC AAC ATA	270
	Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Asn Ile	
	80 85 90	
35	AAG CAA GAT GGA AGT GAG AAA TAC TAT GTG GAC TCT GTG	309
	Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val	
	95 100	
40	AAG GGC CGA TTC ACC ATC TCC AGA GAC AAC GCC AAG AAC	348
	Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn	
	105 110 115	
	TCA CTG TAT CTG CAA ATG AAC AGC CTG AGA GCC GAG GAC	387
45	Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp	
	120 125	
	ACG GCT GTG TAT TAC TGT GCG AGA GAT CTT TTA AAG GTC	426
	Thr Ala Val Tyr Tyr Cys Ala Arg Asp Leu Leu Lys Val	
50	130 135 140	
	AAG GGC AGC TCG TCT GGG TGG TTC GAC CCC TGG GGG AGA	465
	Lys Gly Ser Ser Ser Gly Trp Phe Asp Pro Trp Gly Arg	
	145 150 155	
55	GGG ACC ACG GTC ACC GTC TCG AGT GGT GGA GGC GGT TCA	504
	Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser	
	160 165	
60	GGC GGA GGT GGT AGC GGC GGT GGC GGA TCG TCT GAG CTG	543
	Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu Leu	
	170 175 180	
	ACT CAG GAC CCT GCT GTG TCT GTG GCC TTG GGA CAG ACA	582

Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr
185 190

5 GTC AGG ATC ACA TGC CAA GGA GAC AGC CTC AGA AGC TAT 621
Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr
195 200 205

10 TAT GCA AGC TGG TAC CAG CAG AAG CCA GGA CAG GCC CCT 660
Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
210 215 220

GTA CTT GTC ATC TAT GGT AAA AAC AAC CCG CCC TCA GGG 699
Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly
225 230

15 ATC CCA GAC CGA TTC TCT GGC TCC AGC TCA GGA AAC ACA 738
Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr
235 240 245

20 GCT TCC TTG ACC ATC ACT GGG GCT CAG GCG GAA GAT GAG 777
Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu
250 255

25 GCT GAC TAT TAC TGT AAC TCC CGG GAC AGC AGT GGT AAC 816
Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn
260 265 270

30 CAT GTG GTA TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA 855
His Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
275 280 285

GGT GCG GCC GCA CAT CAT CAT CAC CAT CAC GGG GCC GCA 894
Gly Ala Ala Ala His His His His His His Gly Ala Ala
290 295

35 GAA CAA AAA CTC ATC TCA GAA GAG GAT CTG AAT GGG GCC 933
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala
300 305 310

40 GCA TAG 939
Ala
312

(2) INFORMATION FOR SEQ ID NO:8:

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 933 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
50 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

55

ATG ACC ATG ATT ACG CCA AGC TTT GGA GCC TTT TTT 36
Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe
1 5 10

60

TTG GAG ATT TTC AAC GTG AAA AAA TTA TTA TTC GCA ATT 75
Leu Glu Ile Phe Asn Val Lys Lys Leu Leu Phe Ala Ile
15 20 25

CCT TTA GTT GTT CCT TTC TAT GCG GCC CAG CCG GCC ATG 114
Pro Leu Val Val Pro Phe Tyr Ala Ala Gln Pro Ala Met

30

35

5 GCC CAG GTG CAG CTG GTG CAG TCT GGG GGA GGC GTG GTC 153
 Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val
 40 45 50

10 CAG CCT GGG CGG TCC CTG AGA CTC TCC TGT GCA GCT TCT 192
 Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser
 55 60

15 GGG TTC ATT TTC AGT AGT TAT GGG ATG CAC TGG GTC CGC 231
 Gly Phe Ile Phe Ser Ser Tyr Gly Met His Trp Val Arg
 65 70 75

20 CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG GCA GGT ATT 270
 Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Gly Ile
 80 85 90

25 TTT TAT GAT GGA GGT AAT AAA TAC TAT GCA GAC TCC GTG 309
 Phe Tyr Asp Gly Gly Asn Lys Tyr Tyr Ala Asp Ser Val
 95 100

30 AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC 348
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
 105 110 115

35 ACG CTG TAT CTG CAA ATG AAC AGC CTG AGA GCT GAG GAC 387
 Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
 120 125

40 ACG GCT GTG TAT TAC TGT GCG AGA GAT AGG GGC TAC TAC 426
 Thr Ala Val Tyr Tyr Cys Ala Arg Asp Arg Gly Tyr Tyr
 130 135 140

45 TAC ATG GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC 465
 Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val
 145 150 155

50 TCC TCA GGT GGA GGC GGT TCA GGC GGA GGT GGC TCT GGC 504
 Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 160 165

55 GGT GGC GGA TCG CAG TCT GTG TTG ACG CAG CCG CCC TCA 543
 Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser
 170 175 180

60 GTG TCT GGG GCC CCA GGA CAG AGG GTC ACC ATC TCC TGC 582
 Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys
 185 190

65 ACT GGG AGA AGC TCC AAC ATC GGG GCA GGT CAT GAT GTA 621
 Thr Gly Arg Ser Ser Asn Ile Gly Ala Gly His Asp Val
 195 200 205

70 CAC TGG TAC CAG CAA CTT CCA GGA ACA GCC CCC AAA CTC 660
 His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
 210 215 220

75 CTC ATC TAT GAT GAC AGC AAT CGG CCC TCA GGG GTC CCT 699
 Leu Ile Tyr Asp Asp Ser Asn Arg Pro Ser Gly Val Pro
 225 230

80 GAC CGA TTC TCT GGC TCC AGG TCT GGC ACC TCA GCC TCC 738
 Asp Arg Phe Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser

235 240 245

CTG GCC ATC ACT GGG CTC CAG GCT GAA GAT GAG GCT GAT 777
 Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp
 5 250 255

TAT TAC TGC CAG TCC TAT GAC AGC AGC CTG AGG GGT TCG 816
 Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser Leu Arg Gly Ser
 10 260 265 270

GTA TTC GGC GGA GGG ACC AAG GTC ACT GTC CTA GGT GCG 855
 Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Ala
 275 280 285

GCC GCA CAT CAT CAT CAC CAT CAC GGG GCC GCA GAA CAA 894
 Ala Ala His His His His His His Gly Ala Ala Glu Gln
 15 290 295

AAA CTC ATC TCA GAA GAG GAT CTG AAT GGG GCC GCA 930
 Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala
 20 300 305 310

TAG 933

25 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 309 amino acids
 (B) TYPE: Amino Acid
 30 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile
 35 1 5 10 15

Phe Asn Val Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro
 20 25 30

Phe Tyr Ala Ala Gln Pro Ala Met Ala Glu Val Gln Leu Val Gln
 35 40 45

Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser
 45 50 55 60

Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp
 65 70 75

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile
 50 80 85 90

Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
 95 100 105

Arg Val Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 110 115 120

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 125 130 135

Ala Lys Ile Leu Gly Ala Gly Arg Gly Trp Tyr Phe Asp Leu Trp
 140 145 150

Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser

	155	160	165
	Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu Leu Thr Gln		
	170	175	180
5	Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr		
	185	190	195
	Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln		
10	200	205	210
	Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn		
	215	220	225
15	Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser		
	230	235	240
	Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp		
	245	250	255
20	Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His		
	260	265	270
	Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala Ala		
25	275	280	285
	Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu Ile		
	290	295	300
30	Ser Glu Glu Asp Leu Asn Gly Ala Ala		
	305	309	

(2) INFORMATION FOR SEQ ID NO:10:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 312 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

	Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile	
	1	15
45	Phe Asn Val Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro	
	20	30
	Phe Tyr Ala Ala Gln Pro Ala Met Ala Gly Val Gln Leu Val Glu	
	35	45
50	Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser	
	50	60
	Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Trp Met Ser Trp	
55	65	75
	Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Asn Ile	
	80	90
60	Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys Gly	
	95	105
	Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu	
	110	120

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 125 130 135
 5 Ala Arg Asp Leu Leu Lys Val Lys Gly Ser Ser Ser Gly Trp Phe
 140 145 150
 Asp Pro Trp Gly Arg Gly Thr Thr Val Thr Val Ser Ser Gly Gly
 155 160 165
 10 Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu
 170 175 180
 Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val
 185 190 195
 15 Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser
 200 205 210
 20 Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
 215 220 225
 Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly
 230 235 240
 25 Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln
 245 250 255
 30 Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser
 260 265 270
 Gly Asn His Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 275 280 285
 35 Gly Ala Ala Ala His His His His His His Gly Ala Ala Glu Gln
 290 295 300
 Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala
 305 310 312

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

50 Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile
 1 5 10 15
 Phe Asn Val Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro
 20 25 30
 55 Phe Tyr Ala Ala Gln Pro Ala Met Ala Gln Val Gln Leu Val Gln
 35 40 45
 60 Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser
 50 55 60
 Cys Ala Ala Ser Gly Phe Ile Phe Ser Ser Tyr Gly Met His Trp
 65 70 75

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Gly Ile
80 85 90

5 Phe Tyr Asp Gly Gly Asn Lys Tyr Tyr Ala Asp Ser Val Lys Gly
95 100 105

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
110 115 120

10 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
125 130 135

Ala Arg Asp Arg Gly Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly
140 145 150

15 Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
155 160 165

20 Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro
170 175 180

Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr
185 190 195

25 Gly Arg Ser Ser Asn Ile Gly Ala Gly His Asp Val His Trp Tyr
200 205 210

Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Asp Asp
215 220 225

30 Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Arg
230 235 240

35 Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu
245 250 255

Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser Leu Arg
260 265 270

40 Gly Ser Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Ala
275 280 285

Ala Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu
290 295 300

45 Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala
305 310

(2) INFORMATION FOR SEQ ID NO:12:

50

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

60 AGCGGATAAC AATTTACAC AGG 23

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:

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(2) INFORMATION FOR SEQ ID NO:14:

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

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